

## Widespread dynamic DNA methylation in response to biotic stress.

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**Authors:** R H Downen, M Pelizzola, R J Schmitz, R Lister, J M Downen, J R Nery, J E Dixon, J R Ecker

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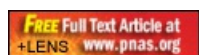
### Public Summary:

Regulation of gene expression by DNA methylation is crucial for defining cellular identities and coordinating organism-wide developmental programs in many organisms. In plants, modulation of DNA methylation in response to environmental conditions represents a potentially robust mechanism to regulate gene expression networks; however, examples of dynamic DNA methylation are largely limited to gene imprinting. Here we report an unexpected role for DNA methylation in regulation of the *Arabidopsis thaliana* immune system. Profiling the DNA methylomes of plants exposed to bacterial pathogen, avirulent bacteria, or salicylic acid (SA) hormone revealed numerous stress-induced differentially methylated regions, many of which were intimately associated with differentially expressed genes. In response to SA, transposon-associated differentially methylated regions, which were accompanied by up-regulation of 21-nt siRNAs, were often coupled to transcriptional changes of the transposon and/or the proximal gene. Thus, dynamic DNA methylation changes within repetitive sequences or transposons can regulate neighboring genes in response to SA stress.

### Scientific Abstract:

Regulation of gene expression by DNA methylation is crucial for defining cellular identities and coordinating organism-wide developmental programs in many organisms. In plants, modulation of DNA methylation in response to environmental conditions represents a potentially robust mechanism to regulate gene expression networks; however, examples of dynamic DNA methylation are largely limited to gene imprinting. Here we report an unexpected role for DNA methylation in regulation of the *Arabidopsis thaliana* immune system. Profiling the DNA methylomes of plants exposed to bacterial pathogen, avirulent bacteria, or salicylic acid (SA) hormone revealed numerous stress-induced differentially methylated regions, many of which were intimately associated with differentially expressed genes. In response to SA, transposon-associated differentially methylated regions, which were accompanied by up-regulation of 21-nt siRNAs, were often coupled to transcriptional changes of the transposon and/or the proximal gene. Thus, dynamic DNA methylation changes within repetitive sequences or transposons can regulate neighboring genes in response to SA stress.

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